

cons.aa	CGGV	AK	E
HTGFER-II	LDTLVGKGRFAEVYKAKLKQNTSEQFETVAVKIFPYDHYASTKDRKDI	FSDINLGHENILQF	
mActR-IIIB	LLEIKARGRFQCVWKAQLAN-----DFVAVKIKPLQDKQSWQSEREI	FSTPGQDHENILQF	
mActR-II	LLEVKARGRFQCVWKAQLLN-----EYVAVKIFPIQDKQSWQNEYEVYSI	PGTHENILQF	
daf-1	LKRVGSGRFQGNVSRGDYRG-----EAVAVKVFRAIDEPAPFKEIEI	FETRMGRHPNVLRY	
subdomains	I	II	III IV

HTGFER-II	LTAERKTELCKQYWLITAFHAKGNLQEYLTRHVISWEDLRNVGSSLRGLSHLPSDHTP-C
mActR-IIIB	IAAEYRGSNLEVELALITAFHDKGSLLIDYLKGNII TWNELCHVAETMSRGISYLHEDVPWCR
mActR-II	IGAEYRGSNDVDLALITAFHEKGSLSDFLKANVVSWNELCHIAETMARGLAYLHEDI PGLK
daf-1	IGSDRVDTGFTTELALVIEYHPSGSLHDFLENTVNIETYYNLPRSTASGLAFLHNQIGGSK
subdomains	V VI-A

cons.aa	DLK N	DFG
HTGFER-II	-GRPKPIVFRDLSSNHLVNDLTCCLCDPGLSLRL---	GPYSSVDDLANSQGVGTARYMAP
mActR-IIIB	GEGHKPSIAFDFAKRVLLYSDLTAVLADPGLAVRF---	EPCGPFGD--THGQVGTARYMAP
mActR-II	-DGHKPAISFDIYSKRVLLYSDLTAVLADPGLALKF---	EAGKSAGD--THGQVGTARYMAP
daf-1	-ESHKPAIAFDIYSKRVLLYSDLTAVLADPGLALKF---	ENYKCGTVRYLAP
subdomains	VI-B	VII VIII

Fig. 1

a.a C C E G N H C
 5' GCGGATCCTGTTGTGAAGGNAATATGTG 3' Fig. 2A
 BAMHI C C G C

a.a V A V K I F
 5' GCGGATCCGTCGCAGTCAAAATTTT 3' Fig. 2B
 BamHI G C G G C
 T T T A

a.a R D I K S K N
 5' GCGGATCCGCGATATTAAGCAA 3' Fig. 2C
 BAMHI A C C GTCT
 G A

a.a E P A H Y
 5' CGGAATTCTGGTGCCATATA Fig. 2D
 EcoRI G G G
 A A

[illegible][illegible][illegible]

Fig. 3

[illegible]

ACCR-II
ACCR-118
TSR-II
ISR-I/ALK-S
ALK-1
ALK-2
ALK-3
ALK-4
ALK-6

Fig. 3 contd.

三三

7

VIA

Fig. 3 contd.

K H L T A C I A D F G L A L X F E A G K S A G G D - - T H G Q V G T R R Y H A P E V L E G A C T R - I I
 K S D L T A V L D F G L A V R F E P G K P P G D L A P S G Q V G T R R Y H A P E V L E G A C T R - I I B
 K H D L T C C C I A D L G L A V R H H S Q S D Y L D I C M M P R V G T K R Y H A P E V L E S T R R - I I
 K X N G T C C C I A D L G L A V M H S Q S D Y L D I C M M P R V G T K R Y H A P E V L D T R R - I / A L K - S
 K S N G Q C C I A D L G L A V M H S Q S D Y L D I C M M P R V G T K R Y H A P E V L D E A L K - 1
 K K N G S C C I A D L G L A V K F N S D Y L D I C M M P R V G T K R Y H A P E V L D E A L K - 2
 K K M G S C C I A D L G L A V K F N S D Y L D I C M M P R V G T K R Y H A P E V L D E A L K - 3
 K K M G S C C I A D L G L A V K F N S D Y L D I C M M P R V G T K R Y H A P E V L D E A L K - 4
 K K M G S C C I A D L G L A V K F N S D Y L D I C M M P R V G T K R Y H A P E V L D E A L K - 6

VIII

VII

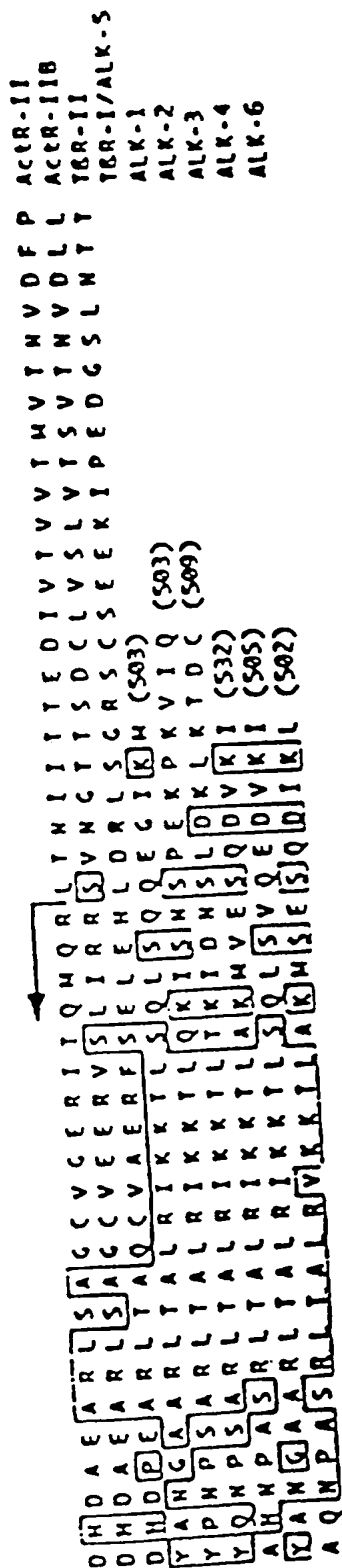
A I M F Q R - D A F L R I I D H Y A M G L V L W E L A S R C T A A D G P P V D E Y M L P P F E E A C T R - I I
 A I M F Q R - D A F L R I I D H Y A M G L V L W E L A S R C T A A D G P P V D E Y M L P P F E E A C T R - I I B
 R M L E N A E S F K Q I D Y Y S M A L V L W E L A S R C T A A D G P P V D E Y M L P P F E E A C T R - I I
 S I N H K H F E S F K R A D I Y A M G L V L W E L A S R C T A A D G P P V D E Y M L P P F E E A C T R - I I
 Q I R T D C F E S Y K T T O I M A F G L V L W E L A S R C T A A D G P P V D E Y M L P P F E E A C T R - I I
 T I T O V D C F E S Y K R V D I M A F G L V L W E L A S R C T A A D G P P V D E Y M L P P F E E A C T R - I I
 S L N K H H F F Q P Y I M A D I Y S E G L I I W E L A S R C T A A D G P P V D E Y M L P P F E E A C T R - I I
 T I N M K H F F Q P Y I M A D I Y S E G L I I W E L A S R C T A A D G P P V D E Y M L P P F E E A C T R - I I
 S L N R M H F F Q P Y I M A D I Y S E G L I I W E L A S R C T A A D G P P V D E Y M L P P F E E A C T R - I I

X

IX

E I G Q H P S L E E D H Q E V V V H K X K R P V L R D Y M Q K H A G M A M L C E T I E E C W A C T R - I I
 E I G Q H P S L E E D H Q E V V V H K X K R P V L R D Y M Q K H A G M A M L C E T I E E C W A C T R - I I B
 K V R E H P S L E E D H Q E V V V H K X K R P V L R D Y M Q K H A G M A M L C E T I E E C W T R R - I I
 L V P S D P S L E E D H Q E V V V H K X K R P V L R D Y M Q K H A G M A M L C E T I E E C W T R R - I / A L K - S
 V V P P N D P S L E E D H Q E V V V H K X K R P V L R D Y M Q K H A G M A M L C E T I E E C W A L K - 1
 V V P P N D P S L E E D H Q E V V V H K X K R P V L R D Y M Q K H A G M A M L C E T I E E C W A L K - 2
 M V P S D P S L E E D H Q E V V V H K X K R P V L R D Y M Q K H A G M A M L C E T I E E C W A L K - 3
 L V P S D P S L E E D H Q E V V V H K X K R P V L R D Y M Q K H A G M A M L C E T I E E C W A L K - 4
 L V P S D P S L E E D H Q E V V V H K X K R P V L R D Y M Q K H A G M A M L C E T I E E C W A L K - 6

Fig. 3 contd.



XI

P K E S S L (S13) A C T R - I I
 P K E S S I (S36) A C T R - I I B
 K (S67) T B R - I I

Fig. 3 contd.

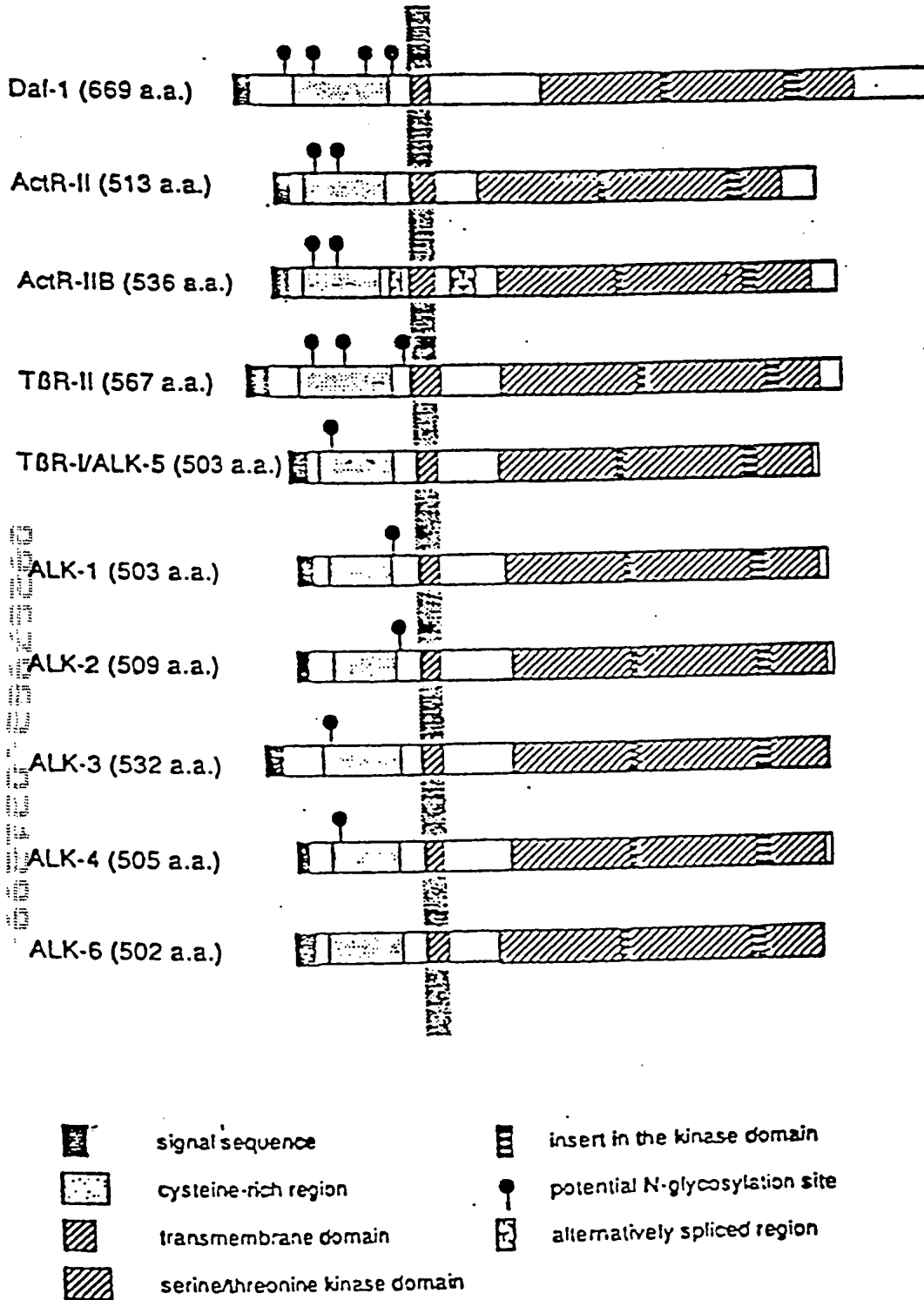


Fig. 4

Fig. 5

ALK-2	ALK-3	ALK-4	ALK-5	ActR-II	ActR-IIB	TβR-II	dal-1	
79	60	61	63	40	40	37	39	ALK-1
	63	64	65	41	39	37	39	ALK-2
		63	65	41	38	37	39	ALK-3
			90	41	40	39	42	ALK-4
				42	40	41	43	ALK-5
					78	48	35	ActR-II
						47	32	ActR-IIB
							34	TβR-II

Fig. 6

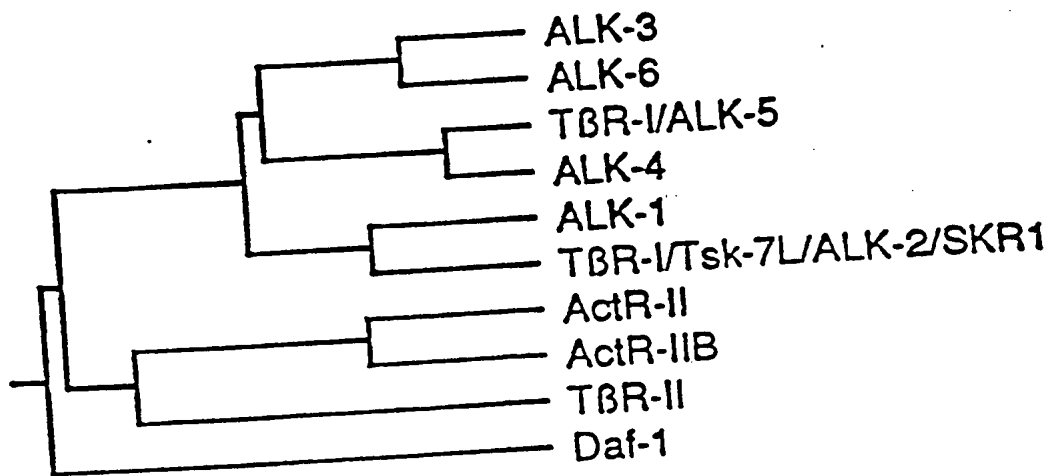


Fig. 7

FLAG-Smad5	-	+	+	+
c.a. ALK1-HA	-	-	+	-
c.a. ALK5-HA	-	-	-	+

IP : anti-FLAG
Blot : anti-phosphoserine

IP : anti-FLAG
Blot : anti-FLAG

IP : (-)
Blot : anti-HA

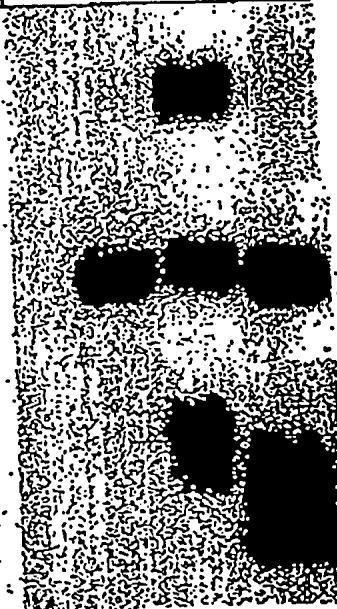


Fig. 8